

RAW SEQUENCE LISTING

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Application Serial Number: 10/537,767
Source: IFWO
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RAW SEQUENCE LISTING

DATE: 05/18/2006

PATENT APPLICATION: US/10/537,767

TIME: 13:47:13

Input Set : A:\10-537,767 Sequence Listing.txt

Output Set: N:\CRF4\05182006\J537767.raw

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3 <110> APPLICANT: Astellas Pharma Inc.
5 <120> TITLE OF INVENTION: Protein Which Binds To Akt2
7 <130> FILE REFERENCE: Q88255
9 <140> CURRENT APPLICATION NUMBER: 10/537,767
10 <141> CURRENT FILING DATE: 2005-06-06
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/15546
13 <151> PRIOR FILING DATE: 2003-12-04
15 <150> PRIOR APPLICATION NUMBER: JP 2002-354155
16 <151> PRIOR FILING DATE: 2002-12-05
18 <150> PRIOR APPLICATION NUMBER: JP 2003-206952
19 <151> PRIOR FILING DATE: 2003-08-08
21 <160> NUMBER OF SEQ ID NOS: 27
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1722
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus sp.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1719)
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37 Met Ala Ala Val Pro Pro Leu Arg Asp Arg Leu Ser Phe Leu His Arg
38 1          5          10          15
40 ctc ccc atc ctg ttg aag ggg acc tca gat gat agc atc cca tgt cca      96
41 Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Ser Ile Pro Cys Pro
42          20          25          30
44 ggc tac ctg ttt gaa gag atc gcc aag att tcc cac gag tca cta ggc      144
45 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Leu Gly
46          35          40          45
48 agc agc cag tgc ctg ctg gag tac ctc ctg aac cgt ctg gac agc agc      192
49 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Asn Arg Leu Asp Ser Ser
50          50          55          60
52 tcc ggc cac gtg aag ctc aag gtg cta aag atc ttg ctt tac ctg tgt      240
53 Ser Gly His Val Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
54 65          70          75          80
56 ggt cat ggc tct tcc tcc ttc ctc ctc atc ctc agg aga aac tct gct      288
57 Gly His Gly Ser Ser Ser Phe Leu Leu Ile Leu Arg Arg Asn Ser Ala
58          85          90          95
60 ctc atc caa gaa gcc acg gct ttc tca ggg cct cca gat cct ctt cac      336
61 Leu Ile Gln Glu Ala Thr Ala Phe Ser Gly Pro Pro Asp Pro Leu His
62          100          105          110
64 gga aat agc ttg tac cag aag gtg cgg gcg gct gcc cag gac ctg ggt      384

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65 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
66      115      120      125
68 agc acc ctg ttc tca gat gcc gtg cca cag cct cca tcg cag cca cct      432
69 Ser Thr Leu Phe Ser Asp Ala Val Pro Gln Pro Pro Ser Gln Pro Pro
70      130      135      140
72 cag atc ccg cct ccc gca ggc atg ggc gcc cag gcc aga cct ctt agt      480
73 Gln Ile Pro Pro Pro Ala Gly Met Gly Ala Gln Ala Arg Pro Leu Ser
74 145      150      155      160
76 gcc ctg caa ggc ttc ggc tac acg aag gag agc agc cgg aca ggc tcc      528
77 Ala Leu Gln Gly Phe Gly Tyr Thr Lys Glu Ser Ser Arg Thr Gly Ser
78      165      170      175
80 gca ggt gaa acc ttc ctc tcc acc atc cag agg gcc gca gag gta gtg      576
81 Ala Gly Glu Thr Phe Leu Ser Thr Ile Gln Arg Ala Ala Glu Val Val
82      180      185      190
84 gct aat gct gtg cgt cct gga cct gat aat cct tgt acc aag gga ccc      624
85 Ala Asn Ala Val Arg Pro Gly Pro Asp Asn Pro Cys Thr Lys Gly Pro
86      195      200      205
88 ttg ccg tat ggt gat tcc tac cag cct gca gtg aca cct tca gct agc      672
89 Leu Pro Tyr Gly Asp Ser Tyr Gln Pro Ala Val Thr Pro Ser Ala Ser
90      210      215      220
92 cac aca cat ccc aac cct ggg aat cta ctc cct ggg gcc atc ctg ggg      720
93 His Thr His Pro Asn Pro Gly Asn Leu Leu Pro Gly Ala Ile Leu Gly
94 225      230      235      240
96 gcc aga gct gtg aga cac cag ccc ggg cag gct ggg ggc ggc tgg gat      768
97 Ala Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp Asp
98      245      250      255
100 gag ctg gac agc agt cct agt tcc cag aat tcc tcc tgc acc agc aac      816
101 Glu Leu Asp Ser Ser Pro Ser Ser Gln Asn Ser Ser Cys Thr Ser Asn
102      260      265      270
104 ctg agc agg gcc tcg gac tcg ggc agt cgg tct ggc agt gac agc cac      864
105 Leu Ser Arg Ala Ser Asp Ser Gly Ser Arg Ser Gly Ser Asp Ser His
106      275      280      285
108 tct ggc acc agc cgg gag cca ggc gac ctg gca gaa agg gct gag gcc      912
109 Ser Gly Thr Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Ala Glu Ala
110      290      295      300
112 acg ccc cca aat gac tgc cag caa gaa ctg aat cta gtg agg act gtg      960
113 Thr Pro Pro Asn Asp Cys Gln Gln Glu Leu Asn Leu Val Arg Thr Val
114 305      310      315      320
116 aca cag ggg cca cgt gtc ttc ctg agc cgt gag gag acg cag cac ttc      1008
117 Thr Gln Gly Pro Arg Val Phe Leu Ser Arg Glu Glu Thr Gln His Phe
118      325      330      335
120 atc aaa gag tgt ggc ctg ctc aac tgt gag gca gtg ctg gag ctg ctc      1056
121 Ile Lys Glu Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Glu Leu Leu
122      340      345      350
124 ctg cgc cag ctg gtc ggg acc agt gag tgc gag cag atg agg gcg ctg      1104
125 Leu Arg Gln Leu Val Gly Thr Ser Glu Cys Glu Gln Met Arg Ala Leu
126      355      360      365
128 tgt gcc atc gcg tcc ttt ggg agt gct gac ctc ctg cct cag gag cac      1152
129 Cys Ala Ile Ala Ser Phe Gly Ser Ala Asp Leu Leu Pro Gln Glu His

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130      370      375      380
132 gtc ctc ctc ctg tgc cga cag cag ctg cag gaa ctt ggc gcg ggc agc      1200
133 Val Leu Leu Leu Cys Arg Gln Gln Leu Gln Glu Leu Gly Ala Gly Ser
134 385      390      395      400
136 cct gga cct gtg acc aac aaa gcc acc aag atc ctg aga cat ttt gaa      1248
137 Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe Glu
138      405      410      415
140 gcc tcc tgt gga caa cag ctc cct acc cta agg ctc tgt gcc cag ccc      1296
141 Ala Ser Cys Gly Gln Gln Leu Pro Thr Leu Arg Leu Cys Ala Gln Pro
142      420      425      430
144 aac tct gca gct gcc cct gtg ggc cca gct gac ctg ctg acc agc ccc      1344
145 Asn Ser Ala Ala Pro Val Gly Pro Ala Asp Leu Leu Thr Ser Pro
146      435      440      445
148 gtg cct gcc cct ggg agc cag gtc ctg ctc cag cct ctc agc tcc gcc      1392
149 Val Pro Ala Pro Gly Ser Gln Val Cys Leu Gln Pro Leu Ser Ser Ala
150      450      455      460
152 aca gtg gta ccc agg agt cct gtg ctc ttt cca tcc ccc aat acc tta      1440
153 Thr Val Val Pro Arg Ser Pro Val Leu Phe Pro Ser Pro Asn Thr Leu
154 465      470      475      480
156 cct ccg tct gct ctg gag gag ccc agc gag gtc cga acc caa ttg gtg      1488
157 Pro Pro Ser Ala Leu Glu Glu Pro Ser Glu Val Arg Thr Gln Leu Val
158      485      490      495
160 tgt tct agt gaa cag ggg aca gaa tct gag cag agg ctg gag aac aca      1536
161 Cys Ser Ser Glu Gln Gly Thr Glu Ser Glu Gln Arg Leu Glu Asn Thr
162      500      505      510
164 gac acc cca gag gat agc tcc agt ccg ctc ccg tgg agt ccc aac tct      1584
165 Asp Thr Pro Glu Asp Ser Ser Ser Pro Leu Pro Trp Ser Pro Asn Ser
166      515      520      525
168 ttg ttt gct ggc atg gag ctg gtg gct tgc ccc cgc ctg cct tgc cac      1632
169 Leu Phe Ala Gly Met Glu Leu Val Ala Cys Pro Arg Leu Pro Cys His
170      530      535      540
172 agc tcg cag gac ctc cag aca gat tta cag aag gtg acc aca gaa gct      1680
173 Ser Ser Gln Asp Leu Gln Thr Asp Leu Gln Lys Val Thr Thr Glu Ala
174 545      550      555      560
176 ccg gtt tca gag cca tca gct ttt gca ttt tta aac atg tga      1722
177 Pro Val Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn Met
178      565      570
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 573
183 <212> TYPE: PRT
184 <213> ORGANISM: Mus sp.
186 <400> SEQUENCE: 2
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189 1      5      10      15
192 Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Ser Ile Pro Cys Pro
193      20      25      30
196 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Leu Gly
197      35      40      45
200 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Asn Arg Leu Asp Ser Ser

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201      50      55      60
204 Ser Gly His Val Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
205 65      70      75      80
208 Gly His Gly Ser Ser Ser Phe Leu Leu Ile Leu Arg Arg Asn Ser Ala
209      85      90      95
212 Leu Ile Gln Glu Ala Thr Ala Phe Ser Gly Pro Pro Asp Pro Leu His
213      100      105      110
216 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
217      115      120      125
220 Ser Thr Leu Phe Ser Asp Ala Val Pro Gln Pro Pro Ser Gln Pro Pro
221      130      135      140
224 Gln Ile Pro Pro Pro Ala Gly Met Gly Ala Gln Ala Arg Pro Leu Ser
225 145      150      155      160
228 Ala Leu Gln Gly Phe Gly Tyr Thr Lys Glu Ser Ser Arg Thr Gly Ser
229      165      170      175
232 Ala Gly Glu Thr Phe Leu Ser Thr Ile Gln Arg Ala Ala Glu Val Val
233      180      185      190
236 Ala Asn Ala Val Arg Pro Gly Pro Asp Asn Pro Cys Thr Lys Gly Pro
237      195      200      205
240 Leu Pro Tyr Gly Asp Ser Tyr Gln Pro Ala Val Thr Pro Ser Ala Ser
241      210      215      220
244 His Thr His Pro Asn Pro Gly Asn Leu Leu Pro Gly Ala Ile Leu Gly
245 225      230      235      240
248 Ala Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp Asp
249      245      250      255
252 Glu Leu Asp Ser Ser Pro Ser Ser Gln Asn Ser Ser Cys Thr Ser Asn
253      260      265      270
256 Leu Ser Arg Ala Ser Asp Ser Gly Ser Arg Ser Gly Ser Asp Ser His
257      275      280      285
260 Ser Gly Thr Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Ala Glu Ala
261      290      295      300
264 Thr Pro Pro Asn Asp Cys Gln Gln Glu Leu Asn Leu Val Arg Thr Val
265 305      310      315      320
268 Thr Gln Gly Pro Arg Val Phe Leu Ser Arg Glu Glu Thr Gln His Phe
269      325      330      335
272 Ile Lys Glu Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Glu Leu Leu
273      340      345      350
276 Leu Arg Gln Leu Val Gly Thr Ser Glu Cys Glu Gln Met Arg Ala Leu
277      355      360      365
280 Cys Ala Ile Ala Ser Phe Gly Ser Ala Asp Leu Leu Pro Gln Glu His
281      370      375      380
284 Val Leu Leu Leu Cys Arg Gln Gln Leu Gln Glu Leu Gly Ala Gly Ser
285 385      390      395      400
288 Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe Glu
289      405      410      415
292 Ala Ser Cys Gly Gln Gln Leu Pro Thr Leu Arg Leu Cys Ala Gln Pro
293      420      425      430
296 Asn Ser Ala Ala Ala Pro Val Gly Pro Ala Asp Leu Leu Thr Ser Pro
297      435      440      445

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300 Val Pro Ala Pro Gly Ser Gln Val Cys Leu Gln Pro Leu Ser Ser Ala
301      450      455      460
304 Thr Val Val Pro Arg Ser Pro Val Leu Phe Pro Ser Pro Asn Thr Leu
305 465      470      475      480
308 Pro Pro Ser Ala Leu Glu Glu Pro Ser Glu Val Arg Thr Gln Leu Val
309      485      490      495
312 Cys Ser Ser Glu Gln Gly Thr Glu Ser Glu Gln Arg Leu Glu Asn Thr
313      500      505      510
316 Asp Thr Pro Glu Asp Ser Ser Ser Pro Leu Pro Trp Ser Pro Asn Ser
317      515      520      525
320 Leu Phe Ala Gly Met Glu Leu Val Ala Cys Pro Arg Leu Pro Cys His
321      530      535      540
324 Ser Ser Gln Asp Leu Gln Thr Asp Leu Gln Lys Val Thr Thr Glu Ala
325 545      550      555      560
328 Pro Val Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn Met
329      565      570
332 <210> SEQ ID NO: 3
333 <211> LENGTH: 1782
334 <212> TYPE: DNA
335 <213> ORGANISM: Homo sapiens
338 <220> FEATURE:
339 <221> NAME/KEY: CDS
340 <222> LOCATION: (1)..(1782)
342 <400> SEQUENCE: 3
343 atg gct gcc gcg ccg ccg cta cgg gac cgc ctg agc ttt cta cac cgg      48
344 Met Ala Ala Ala Pro Pro Leu Arg Asp Arg Leu Ser Phe Leu His Arg
345 1      5      10      15
347 ctg ccg att ctg ctg aag ggg acg tcc gat gat gat gtc ccg tgt ccg      96
348 Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Asp Val Pro Cys Pro
349      20      25      30
351 ggc tac ctg ttt gaa gag att gct aaa atc tcc cac gag tct ccg ggc      144
352 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Pro Gly
353      35      40      45
355 agc agc cag tgc ctg ctg gag tac ctg ctg agc cgc ctg cac agc agc      192
356 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Ser Arg Leu His Ser Ser
357      50      55      60
359 tcc ggc cac ggg aag ctg aag gtg ctg aag atc ctg ctg tat ctg tgc      240
360 Ser Gly His Gly Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
361 65      70      75      80
363 agc cac ggc tcc tcc ttc ttc ctg ctg atc ctg aaa cgc aac tct gcc      288
364 Ser His Gly Ser Ser Phe Phe Leu Leu Ile Leu Lys Arg Asn Ser Ala
365      85      90      95
367 ttc atc cag gaa gct gca gct ttt gca ggg ccc cca gat cct ctg cac      336
368 Phe Ile Gln Glu Ala Ala Ala Phe Ala Gly Pro Pro Asp Pro Leu His
369      100      105      110
371 ggg aac agc ttg tac cag aag gtt cgc gcg gcc gcg cag gac ttg ggg      384
372 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
373      115      120      125
375 agc acc ctg ttc tcg gac acc gtg ttg ccg ctg gct ccc tcc cag cct      432

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VERIFICATION SUMMARY

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